EXHIBIT 1

John Rickert Devereux
49 Chequamegon Bay Drive
Madison, Wisconsin, 53719
(608) 277-9203
john.devereux@pobox.com

EDUCATION

B.A.	University of Wisconsin-Madison	1970	History
M.S.	University of Wisconsin-Madison	1981	Botany
Ph.D.	University of Wisconsin-Madison	1988	Computational Genetics

PROFESSIONAL EXPERIENCE

1997-2000, President and Chief Scientific Officer, Genetics Computer Group, Inc. (GCG), a wholly owned subsidiary of Oxford Molecular Group, PLC.

1990-1997, President and Founder, Genetics Computer Group, Inc. (GCG).

1985-1989, Assistant Director, University of Wisconsin Biotechnology Center.

1977-1985, Project Coordinator, University of Wisconsin Department of Genetics.

ACADEMIC SERVICE (1990s only)

Ad hoc DOE review panels for the Human Genome Program (3 times)
Ad hoc NIH review panels for the Human Genome Program (5 times)
NIH/DOE Human Genome Joint Informatics Task Force (1989-91)
NIH/DOE Human Genome DNA Sequencing Working Group (1990-92)
National Center for Biotechnology Information (NCBI)
Board of Scientific Councilors (BOSC) (1990-94)

HONORS

EMBL Sabbatical Fellowship (1984)
EMBO Lectureship (1985)
EMBO Lectureship (1989)

PUBLICATIONS

1. Smithies, O., Engels, W.R., Devereux, J.R., Slightom, J.L., and Shen, S. (1981). Base substitutions, length differences and DNA strand asymmetries in the human G-Gamma and A-Gamma fetal globin gene region, *Cell* **26**, 345-353. (Published together with:)

2. Shen, S., Slightom, J.L., and Smithies, O. (1981). A history of the human fetal globin gene duplication, *Cell* **26**, 191-203.)

3. Squires, C.H., DeFelice, M., Devereux, J., and Calvo, J.M. (1983). Molecular structure of ilvIH and its evolutionary relationship to ilvG in Escherichia coli K12, *Nucleic Acids Research* **11(15)**, 5299-5311.

4. Pedersen, K., Devereux, J., Wilson, D.R., Sheldon, E., and Larkins, B.A. (1982). Cloning and sequence analysis reveal structural variation among related Zein genes in maize, *Cell* **29**, 1015-1026.

5. Devereux, J., Haeberli, P., and Smithies, O. (1984). A Comprehensive Set of Sequence Analysis Programs for the VAX, *Nucleic Acids Research* **12(1)**, 387-395. *

6. Gribskov, M., Devereux, J., and Burgess, R.R. (1984). The codon preference plot: Graphic analysis of protein coding sequences and prediction of gene expression, *Nucleic Acids Research* **12(1)**, 539-549.

7. Gribskov, M., Burgess, R.R., and Devereux, J. (1986). PEPPLOT, a protein secondary structure analysis program for the UWGCG Sequence Analysis Software Package, *Nucleic Acids Research* **14(1)**, 327-334.

8. Devereux, J. (1988). A rapid method for identifying sequences in large nucleotide sequence databases, a doctoral thesis available from University Microfilms Inc., Ann Arbor, Michigan, USA.

9. Gribskov, M., Devereux, J.; editors, (1991). *A Sequence Analysis Primer*, Stockton Press, New York, NY, USA.

10. Devereux, J. (1995). *The GCG Sequence Analysis Software Package, Version 8.0*, Genetics Computer Group, Inc., University Research Park, 575 Science Drive, Madison, Wisconsin, USA, 53711. **

11. Devereux, J. (1995). *The GCG Procedure Library, Version 8.0*, Genetics Computer Group, Inc., University Research Park, 575 Science Drive, Madison, Wisconsin, USA, 53711.

* According to Guardian Unlimited (guardian.co.uk, Sept 25, 2003), the online version of the *Manchester Guardian*, this paper was then the fifth most-cited paper in all of science.

** The Wisconsin Package™ had eight major releases with Devereux as the senior author: Version 1.0, March, 1983, Version 2.0, June, 1984, Version 3.0, June, 1985, Version 4.0, June, 1986, Version 5.0, June, 1987, Version 6.0, June, 1989, Version 7.0, June, 1991. After 1995, others at GCG were more central to the enhancing and updating this venerable software package.

EXHIBIT 2

SPEZYME® ETHYL AMINO ACID SEQUENCE

```
  1 AAPFNGTMMQ YFEWYLPDDG TLWTKVANEA NNLSSLGITA LWLPPAYKGT SRSDVGYGVY
 61 DLYDLGEFNQ KGTVRTKYGT KAQYLQAIQA AHAAGMQVYA DVVFDHKGGA DGTEWVDAVE
121 VNPSDRNQEI SGTYQIQAWT KFDFPGRGNT YSSFKWRWYH FDGVDWDESR KLSRIYKFIG
181 KAWDWEVDTE NGNYDYLMYA DLDMDHPEVV TELKNWGKWY VNTTNIDGFR LDAVKHIKFS
241 FFPDWLSYVR SQTGKPLFTV GEYWSYDINK LHNYITKTNG TMSLFDAPLH NKFYTASKSG
301 GAFDMRTLMT NTLMKDQPTL AVTFVDNHDT EPGQALQSWV DPWFKPLAYA FILTRQEGYP
361 CVFYGDYYGI PQYNIPSLKS KIDPLLIARR DYAYGTQHDY LDHSDIIGWT REGVTEKPGS
421 GLAALITDGP GGSKWMYVGK QHAGKVFYDL TGNRSDTVTI NSDGWGEFKV NGGSVSVWVP
481 RKTT
```

EXHIBIT 3

GAP ALIGNMENT:
SEQ ID NO:3 to Spezyme Ethyl (Old Matrix)

GAP of: NewB.pep check: 1170 from: 1 to: 514

WPDEF Seq ID Nos 3, translated by ThreeToOne
none

to: SPEZE.pep check: 525 from: 1 to: 484

WPDEF SPEZYME® ETHYL AMINO ACID SEQUENCE
None

Symbol comparison table: oldpep.cmp CompCheck: 2543
Dayhoff table (Schwartz, R. M. and Dayhoff, M. O. [1979] in Atlas of Protein Sequence and Structure, Dayhoff, M. O. Ed, pp. 353-358, National Biomedical Research Foundation, Washington D.C.) rescaled by dividing each value by the sum of its row and column, and normalizing to a mean of 0 and standard deviation of 1.0. The value for FY (Phe-Tyr) = RW = 1.425. Perfect matches are set to 1.5 and no matches on any row are . . .

Gap Weight:	30	Average Match:	5.402
Length Weight:	3	Average Mismatch:	-3.964
Quality:	7155	Length:	514
Ratio:	14.783	Gaps:	1
Percent Similarity:	99.380	Percent Identity:	98.967

Match display thresholds for the alignment(s):
| = IDENTITY
: = 4
. = 1

NewB.pep x SPEZE.pep June 3, 2005 11:08 ..

```
                .         .         .         .         .
      1 AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGT 50
        ||||||||||||||||||||||||||||||||||||||||||||||||||
      1 AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGT 50
                .         .         .         .         .
     51 SRSDVGYGVYDLYDLGEFNQKGAVRTKYGTKAQYLQAIQAAHAAGMQVYA 100
        ||||||||||||||||||||||:||||||||||||||||||||||||||||
     51 SRSDVGYGVYDLYDLGEFNQKGTVRTKYGTKAQYLQAIQAAHAAGMQVYA 100
                .         .         .         .         .
    101 DVVFDHKGGADGTEWVDAVEVNPSDRNQEISGTYQIQAWTKFDFPGRGNT 150
        ||||||||||||||||||||||||||||||||||||||||||||||||||||
    101 DVVFDHKGGADGTEWVDAVEVNPSDRNQEISGTYQIQAWTKFDFPGRGNT 150
                .         .         .         .         .
    151 YSSFKWRWYHFDGVDWDESRKLSRIYKFRGIGKAWDWEVDTENGNYDYLM 200
        |||||||||||||||||||||||||||||  ||||||||||||||||||||
    151 YSSFKWRWYHFDGVDWDESRKLSRIYKF..IGKAWDWEVDTENGNYDYLM 198
                .         .         .         .         .
    201 YADLDMDHPEVVTELKSWGKWYVNTTNIDGFRLDAVKHIKFSFFPDWLSD 250
        |||||||||||||||.||||||||||||||||||||||||||||||||||
    199 YADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIKFSFFPDWLSY 248
```

GAP Alignment:
SEQ ID NO:3 to Spezyme Ethyl
(Old Matrix)

```
251 VRSQTGKPLFTVGEYWSYDINKLHNYIMKTNGTMSLFDAPLHNKFYTASK 300
    ||||||||||||||||||||||||||| ||||||||||||||||||||||
249 VRSQTGKPLFTVGEYWSYDINKLHNYITKTNGTMSLFDAPLHNKFYTASK 298

301 SGGTFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLA 350
    |||:||||||||||||||||||||||||||||||||||||||||||||||
299 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLA 348

351 YAFILTRQEGYPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQH 400
    ||||||||||||||||||||||||||||||||||||||||||||||||||
349 YAFILTRQEGYPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQH 398

401 DYLDHSDIIGWTREGVTEKPGSGLAALITDGPGGSKWMYVGKQHAGKVFY 450
    ||||||||||||||||||||||||||||||||||||||||||||||||||
399 DYLDHSDIIGWTREGVTEKPGSGLAALITDGPGGSKWMYVGKQHAGKVFY 448

451 DLTGNRSDTVTINSDGWGEFKVNGGSVSVWVPRKTTVSTIAWSITTRPWT 500
    ||||||||||||||||||||||||||||||||||
449 DLTGNRSDTVTINSDGWGEFKVNGGSVSVWVPRKTT.............. 484
```

Exhibit 4

GAP ALIGNMENT:
SEQ ID NO:3 to Spezyme Ethyl (New Matrix)

GAP of: NewB.pep check: 1170 from: 1 to: 514

WPDEF Seq ID Nos 3, translated by ThreeToOne
none

to: SPEZE.pep check: 525 from: 1 to: 484

WPDEF SPEZYME® ETHYL AMINO ACID SEQUENCE
None

Symbol comparison table: blosum62.cmp CompCheck: 1102
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid substitution matrices from protein blocks. Proc. Natl. Acad. Sci. USA 89: 10915-10919.

Gap Weight:	8	Average Match:	2.778
Length Weight:	2	Average Mismatch:	-2.248
Quality:	2635	Length:	514
Ratio:	5.444	Gaps:	1
Percent Similarity:	98.967	Percent Identity:	98.967

Match display thresholds for the alignment(s):
| = IDENTITY
: = 2
. = 1

NewB.pep x SPEZE.pep June 3, 2005 11:04 ..

```
                .         .         .         .         .
      1 AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGT 50
        ||||||||||||||||||||||||||||||||||||||||||||||||||
      1 AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGT 50
                .         .         .         .         .
     51 SRSDVGYGVYDLYDLGEFNQKGAVRTKYGTKAQYLQAIQAAHAAGMQVYA 100
        |||||||||||||||||||| ||||||||||||||||||||||||||||
     51 SRSDVGYGVYDLYDLGEFNQKGTVRTKYGTKAQYLQAIQAAHAAGMQVYA 100
                .         .         .         .         .
    101 DVVFDHKGGADGTEWVDAVEVNPSDRNQEISGTYQIQAWTKFDFPGRGNT 150
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    101 DVVFDHKGGADGTEWVDAVEVNPSDRNQEISGTYQIQAWTKFDFPGRGNT 150
                .         .         .         .         .
    151 YSSFKWRWYHFDGVDWDESRKLSRIYKFRGIGKAWDWEVDTENGNYDYLM 200
        |||||||||||||||||||||||||||  ||||||||||||||||||||
    151 YSSFKWRWYHFDGVDWDESRKLSRIYKF..IGKAWDWEVDTENGNYDYLM 198
                .         .         .         .         .
    201 YADLDMDHPEVVTELKSWGKWYVNTTNIDGFRLDAVKHIKFSFFPDWLSD 250
        |||||||||||||||.||||||||||||||||||||||||||||||||||
    199 YADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIKFSFFPDWLSY 248
                .         .         .         .         .
    251 VRSQTGKPLFTVGEYWSYDINKLHNYIMKTNGTMSLFDAPLHNKFYTASK 300
```

GAP Alignment:
SEQ ID NO:3 to Spezyme Ethyl
(New Matrix)

```
                                                                                
249 VRSQTGKPLFTVGEYWSYDINKLHNYITKTNGTMSLFDAPLHNKFYTASK 298
                                                                                
301 SGGTFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLA 350
                                                                                
299 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLA 348
                                                                                
351 YAFILTRQEGYPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQH 400
                                                                                
349 YAFILTRQEGYPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQH 398
                                                                                
401 DYLDHSDIIGWTREGVTEKPGSGLAALITDGPGGSKWMYVGKQHAGKVFY 450
                                                                                
399 DYLDHSDIIGWTREGVTEKPGSGLAALITDGPGGSKWMYVGKQHAGKVFY 448
                                                                                
451 DLTGNRSDTVTINSDGWGEFKVNGGSVSVWVPRKTTVSTIAWSITTRPWT 500
                                                                                
449 DLTGNRSDTVTINSDGWGEFKVNGGSVSVWVPRKTT.............. 484
```

EXHIBIT 5

GAP ALIGNMENT:
Sequence 3 (Figure 1) to Spezyme Ethyl (Old Matrix)

```
 GAP of: NewA.pep  check: 754  from: 1  to: 514

WPDEF A.        Figure 1, sequence 3

 to: SPEZE.pep  check: 525  from: 1  to: 484

WPDEF SPEZYME® ETHYL AMINO ACID SEQUENCE
None

 Symbol comparison table: oldpep.cmp CompCheck: 2543
Dayhoff table (Schwartz, R. M. and Dayhoff, M. O. [1979] in Atlas of
Protein Sequence and Structure, Dayhoff, M. O. Ed, pp. 353-358, National
Biomedical Research Foundation, Washington D.C.) rescaled by dividing
each value by the sum of its row and column, and normalizing to a mean
of 0 and standard deviation of 1.0.  The value for FY (Phe-Tyr) = RW =
1.425.  Perfect matches are set to 1.5 and no matches on any row are . . .

        Gap Weight:     30      Average Match:  5.402
     Length Weight:      3   Average Mismatch: -3.964

           Quality:   7203             Length:    514
             Ratio: 14.882               Gaps:      1
Percent Similarity: 99.793   Percent Identity: 99.587

       Match display thresholds for the alignment(s):
                  | = IDENTITY
                  : =    4
                  . =    1

NewA.pep x SPEZE.pep      June 3, 2005 11:06  ..

                .         .         .         .         .
      1 aapfngtmmqyfewylpddgtlwtkvaneannlsslgitalwlppaykgt 50
        ||||||||||||||||||||||||||||||||||||||||||||||||||
      1 AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGT 50
                .         .         .         .         .
     51 srsdvgygvydlydlgefnqkgtvrtkygtkaqylqaiqaahaagmqvya 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||
     51 SRSDVGYGVYDLYDLGEFNQKGTVRTKYGTKAQYLQAIQAAHAAGMQVYA 100
                .         .         .         .         .
    101 dvvfdhkggadgtewvdavevnpsdrnqeisgtyqiqawtkfdfpgrgnt 150
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    101 DVVFDHKGGADGTEWVDAVEVNPSDRNQEISGTYQIQAWTKFDFPGRGNT 150
                .         .         .         .         .
    151 yssfkwrwyhfdgvdwdesrklsriykfrgigkawdwevdtengnydylm 200
        |||||||||||||||||||||||||||  ||||||||||||||||||||
    151 YSSFKWRWYHFDGVDWDESRKLSRIYKF..IGKAWDWEVDTENGNYDYLM 198
                .         .         .         .         .
    201 yadldmdhpevvtelknwgkwyvnttnidgfrldavkhikfsffpdwlsy 250
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    199 YADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIKFSFFPDWLSY 248
                .         .         .         .         .
```

GAP Alignment:
Sequence 3 (Figure 1) to Spezyme Ethyl
(Old Matrix)

```
251 vrsqtgkplftvgeywsydinklhnyitktdgtmslfdaplhnkfytask 300
    ||||||||||||||||||||||||||||||:||||||||||||||||||||
249 VRSQTGKPLFTVGEYWSYDINKLHNYITKTNGTMSLFDAPLHNKFYTASK 298
              .         .         .         .         .
301 sggafdmrtlmtntlmkdqptlavtfvdnhdtepgqalqswvdpwfkpla 350
    ||||||||||||||||||||||||||||||||||||||||||||||||||
299 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLA 348
              .         .         .         .         .
351 yafiltrqegypcvfygdyygipqynipslkskidplliarrdyaygtqh 400
    ||||||||||||||||||||||||||||||||||||||||||||||||||
349 YAFILTRQEGYPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQH 398
              .         .         .         .         .
401 dyldhsdiigwtreggtekpgsglaalitdgpggskwmyvgkqhagkvfy 450
    ||||||||||||||||.|||||||||||||||||||||||||||||||||
399 DYLDHSDIIGWTREGVTEKPGSGLAALITDGPGGSKWMYVGKQHAGKVFY 448
              .         .         .         .         .
451 dltgnrsdtvtinsdgwgefkvnggsvsvwvprkttvstiarpittrpwt 500
    ||||||||||||||||||||||||||||||||||||
449 DLTGNRSDTVTINSDGWGEFKVNGGSVSVWVPRKTT.............. 484
                                  .
                                  .
                                  .
```

EXHIBIT 6

GAP ALIGNMENT:
Sequence 3 (Figure 1) to Spezyme Ethyl (New Matrix)

```
 GAP of: NewA.pep  check: 754  from: 1  to: 514

WPDEF A.        Figure 1, sequence 3

 to: SPEZE.pep  check: 525  from: 1  to: 484

WPDEF SPEZYME® ETHYL AMINO ACID SEQUENCE
None

 Symbol comparison table: blosum62.cmp CompCheck: 1102
BLOSUM62 amino acid substitution matrix.
Reference: Henikoff, S. and Henikoff, J. G. (1992). Amino acid
           substitution matrices from protein blocks.  Proc. Natl. Acad.
           Sci. USA 89: 10915-10919.

        Gap Weight:      8      Average Match:  2.778
     Length Weight:      2   Average Mismatch: -2.248

           Quality:   2653           Length:    514
             Ratio:  5.481             Gaps:      1
Percent Similarity: 99.587   Percent Identity: 99.587

       Match display thresholds for the alignment(s):
                  | = IDENTITY
                  : =   2
                  . =   1

NewA.pep x SPEZE.pep      June 3, 2005 11:03  ..

                .         .         .         .         .
      1 aapfngtmmqyfewylpddgtlwtkvaneannlsslgitalwlppaykgt 50
        ||||||||||||||||||||||||||||||||||||||||||||||||||
      1 AAPFNGTMMQYFEWYLPDDGTLWTKVANEANNLSSLGITALWLPPAYKGT 50
                .         .         .         .         .
     51 srsdvgygvydlydlgefnqkgtvrtkygtkaqylqaiqaahaagmqvya 100
        ||||||||||||||||||||||||||||||||||||||||||||||||||
     51 SRSDVGYGVYDLYDLGEFNQKGTVRTKYGTKAQYLQAIQAAHAAGMQVYA 100
                .         .         .         .         .
    101 dvvfdhkggadgtewvdavevnpsdrnqeisgtyqiqawtkfdfpgrgnt 150
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    101 DVVFDHKGGADGTEWVDAVEVNPSDRNQEISGTYQIQAWTKFDFPGRGNT 150
                .         .         .         .         .
    151 yssfkwrwyhfdgvdwdesrklsriykfrgigkawdwevdtengnydylm 200
        |||||||||||||||||||||||||||  ||||||||||||||||||||
    151 YSSFKWRWYHFDGVDWDESRKLSRIYKF..IGKAWDWEVDTENGNYDYLM 198
                .         .         .         .         .
    201 yadldmdhpevvtelknwgkwyvnttnidgfrldavkhikfsffpdwlsy 250
        ||||||||||||||||||||||||||||||||||||||||||||||||||
    199 YADLDMDHPEVVTELKNWGKWYVNTTNIDGFRLDAVKHIKFSFFPDWLSY 248
                .         .         .         .         .
    251 vrsqtgkplftvgeywsydinklhnyitktdgtmslfdaplhnkfytask 300
        ||||||||||||||||||||||||||||.||||||||||||||||||||
```

GAP Alignment:
Sequence 3 (Figure 1) to Spezyme Ethyl
(New Matrix)

```
249 VRSQTGKPLFTVGEYWSYDINKLHNYITKTNGTMSLFDAPLHNKFYTASK 298
301 sggafdmrtlmtntlmkdqptlavtfvdnhdtepgqalqswvdpwfkpla 350
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
299 SGGAFDMRTLMTNTLMKDQPTLAVTFVDNHDTEPGQALQSWVDPWFKPLA 348
351 yafiltrqegypcvfygdyygipqynipslkskidplliarrdyaygtqh 400
    ||||||||||||||||||||||||||||||||||||||||||||||||||||
349 YAFILTRQEGYPCVFYGDYYGIPQYNIPSLKSKIDPLLIARRDYAYGTQH 398
401 dyldhsdiigwtreggtekpgsglaalitdgpggskwmyvgkqhagkvfy 450
    |||||||||||||||| ||||||||||||||||||||||||||||||||
399 DYLDHSDIIGWTREGVTEKPGSGLAALITDGPGGSKWMYVGKQHAGKVFY 448
451 dltgnrsdtvtinsdgwgefkvnggsvsvwvprkttvstiarpittrpwt 500
    ||||||||||||||||||||||||||||||||||
449 DLTGNRSDTVTINSDGWGEFKVNGGSVSVWVPRKTT..............  484
```